RAW SEQUENCE LISTING

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Application Serial Number: _10/501,756_

Source: _PCT_

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RAW SEQUENCE LISTING   DATE: 01/04/2005
PATENT APPLICATION: US/10/501,756   TIME: 14:46:48   PCT

Input Set : D:\180-137 PCT.ST25.txt
Output Set: N:\CRF4\01042005\J501756.raw

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   3 <110> APPLICANT: Duke University
   4       Chuan-Yuan, Li
   5       Xiuwu, Zhang
   7 <120> TITLE OF INVENTION: GENERATION OF RECOMBINANT ADENO-ASSOCIATED VIRAL VECTORS BY
A
   8       COMPLETE ADENOVIRUS-MEDIATED APPROACH
  10 <130> FILE REFERENCE: 180/137
C--> 12 <140> CURRENT APPLICATION NUMBER: US/10/501,756
C--> 12 <141> CURRENT FILING DATE: 2004-07-16
  12 <150> PRIOR APPLICATION NUMBER: US 60/349,532
  13 <151> PRIOR FILING DATE: 2002-01-18
  15 <160> NUMBER OF SEQ ID NOS: 22
  17 <170> SOFTWARE: PatentIn version 3.2
  19 <210> SEQ ID NO: 1
  20 <211> LENGTH: 1611
  21 <212> TYPE: DNA
  22 <213> ORGANISM: adeno-associated virus 2
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  26 <221> NAME/KEY: CDS
  27 <222> LOCATION: (1)..(1611)
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  34 gag cat ctg ccc ggc att tct gac agc ttt gtg aac tgg gtg gcc gag       96
  35 Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu
  36              20                  25                  30
  38 aag gaa tgg gag ttg ccg cca gat tct gac atg gat ctg aat ctg att      144
  39 Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile
  40          35                  40                  45
  42 gag cag gca ccc ctg acc gtg gcc gag aag ctg cag cgc gac ttt ctg      192
  43 Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu
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  46 acg gaa tgg cgc cgt gtg agt aag gcc ccg gag gcc ctt ttc ttt gtg      240
  47 Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val
  48 65                  70                  75                  80
  50 caa ttt gag aag gga gag agc tac ttc cac atg cac gtg ctc gtg gaa      288
  51 Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu
  52                  85                  90                  95
  54 acc acc ggg gtg aaa tcc atg gtt ttg gga cgt ttc ctg agt cag att      336
  55 Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile
  56                  100                 105                 110
  58 cgc gaa aaa ctg att cag aga att tac cgc ggg atc gag ccg act ttg      384
  59 Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu
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62 cca aac tgg ttc gcg gtc aca aag acc aga aat ggc gcc gga ggc ggg        432
63 Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly
64        130              135            140
66 aac aag gtg gtg gat gag tgc tac atc ccc aat tac ttg ctc ccc aaa        480
67 Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys
68 145              150            ، 155                160
70 acc cag cct gag ctc cag tgg gcg tgg act aat atg gaa cag tat tta        528
71 Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu
72              165              170              175
74 agc gcc tgt ttg aat ctc acg gag cgt aaa cgg ttg gtg gcg cag cat        576
75 Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His
76        180              185            190
78 ctg acg cac gtg tcg cag acg cag gag cag aac aaa gag aat cag aat        624
79 Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn
80        195              200            205
82 ccc aat tct gat gcg ccg gtg atc aga tca aaa act tca gcc agg tac        672
83 Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr
84        210              215            220
86 atg gag ctg gtc ggg tgg ctc gtg gac aag ggg att acc tcg gag aag        720
87 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
88 225              230            235                240
90 cag tgg atc cag gag gac cag gcc tca tac atc tcc ttc aat gcg gcc        768
91 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
92              245              250              255
94 tcc aac tcg cgg tcc caa atc aag gct gcc ttg gac aat gcg gga aag        816
95 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
96        260              265            270
98 att atg agc ctg act aaa acc gcc ccc gac tac ctg gtg ggc cag cag        864
99 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
100       275              280            285
102 ccc gtg gag gac att tcc agc aat cgg att tat aaa att ttg gaa cta       912
103 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
104       290              295            300
106 aac ggg tac gat ccc caa tat gcg gct tcc gtc ttt ctg gga tgg gcc       960
107 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
108 305              310            315                320
110 acg aaa aag ttc ggc aag agg aac acc atc tgg ctg ttt ggg cct gca      1008
111 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
112              325              330              335
114 act acc ggg aag acc aac atc gcg gag gcc ata gcc cac act gtg ccc      1056
115 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
116       340              345            350
118 ttc tac ggg tgc gta aac tgg acc aat gag aac ttt ccc ttc aac gac      1104
119 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
120       355              360            365
122 tgt gtc gac aag atg gtg atc tgg tgg gag gag ggg aag atg acc gcc      1152
123 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
124       370              375            380
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128 385                 390                 395                 400
130 gtg gac cag aaa tgc aag tcc tcg gcc cag ata gac ccg act ccc gtg        1248
131 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
132                 405                 410                 415
134 atc gtc acc tcc aac acc aac atg tgc gcc gtg att gac ggg aac tca        1296
135 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
136                 420                 425                 430
138 acg acc ttc gaa cac cag cag ccg ttg caa gac cgg atg ttc aaa ttt        1344
139 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
140             435                 440                 445
142 gaa ctc acc cgc cgt ctg gat cat gac ttt ggg aag gtc acc aag cag        1392
143 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
144     450                 455                 460
146 gaa gtc aaa gac ttt ttc cgg tgg gca aag gat cac gtg gtt gag gtg        1440
147 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
148 465                 470                 475                 480
150 gag cat gaa ttc tac gtc aaa aag ggt gga gcc aag aaa aga ccc gcc        1488
151 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
152                 485                 490                 495
154 ccc agt gac gca gat ata agt gag ccc aaa cgg gtg cgc gag tca gtt        1536
155 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
156                 500                 505                 510
158 gcg cag cca tcg acg tca gac gcg gaa gct tcg atc aac tac gca gac        1584
159 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
160             515                 520                 525
162 aga ttg gct cga gga cac tct ctc tga                                    1611
163 Arg Leu Ala Arg Gly His Ser Leu
164     530                 535
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168 <211> LENGTH: 536
169 <212> TYPE: PRT
170 <213> ORGANISM: adeno-associated virus 2
172 <400> SEQUENCE: 2
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179                 20                  25                  30
182 Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile
183             35                  40                  45
186 Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu
187     50                  55                  60
190 Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val
191 65                  70                  75                  80
194 Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu
195                 85                  90                  95
198 Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile
199                 100                 105                 110
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206 Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly
207     130             135             140
210 Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys
211 145             150             155             160
214 Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu
215             165             170             175
218 Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His
219         180             185             190
222 Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn
223         195             200             205
226 Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr
227     210             215             220
230 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
231 225             230             235             240
234 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
235             245             250             255
238 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
239         260             265             270
242 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
243         275             280             285
246 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
247     290             295             300
250 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
251 305             310             315             320
254 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
255             325             330             335
258 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
259         340             345             350
262 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
263         355             360             365
266 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
267     370             375             380
270 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
271 385             390             395             400
274 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
275             405             410             415
278 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
279         420             425             430
282 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
283         435             440             445
286 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
287     450             455             460
290 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
291 465             470             475             480
294 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
295             485             490             495
298 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
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299              500              505              510
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306 Arg Leu Ala Arg Gly His Ser Leu
307      530              535
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311 <211> LENGTH: 1866
312 <212> TYPE: DNA
313 <213> ORGANISM: adeno-associated virus 2
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317 <221> NAME/KEY: CDS
318 <222> LOCATION: (1)..(1866)
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323 1               5                10               15
325 ggg cat ctg ccc ggc att tct gac agc ttt gtg aac tgg gtg gcc gag      96
326 Gly His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu
327          20               25               30
329 aag gaa tgg gag ttg ccg cca gat tct gac atg gat ctg aat ctg att     144
330 Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile
331      35               40               45
333 gag cag gca ccc ctg acc gtg gcc gag aag ctg cag cgc gac ttt ctg     192
334 Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu
335      50               55               60
337 acg gaa tgg cgc cgt gtg agt aag gcc ccg gag gcc ctt ttc ttt gtg     240
338 Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val
339 65               70               75               80
341 caa ttt gag aag gga gag agc tac ttc cac atg cac gtg ctc gtg gaa     288
342 Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu
343          85               90               95
345 acc acc ggg gtg aaa tcc atg gtt ttg gga cgt ttc ctg agt cag att     336
346 Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile
347          100              105              110
349 cgc gaa aaa ctg att cag aga att tac cgc ggg atc gag ccg act ttg     384
350 Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu
351          115              120              125
353 cca aac tgg ttc gcg gtc aca aag acc aga aat ggc gcc gga ggc ggg     432
354 Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly
355      130              135              140
357 aac aag gtg gtg gat gag tgc tac atc ccc aat tac ttg ctc ccc aag     480
358 Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys
359 145              150              155              160
361 acc cag cct gaa ctg cag tgg gcg tgg act aat atg gaa cag tat tta     528
362 Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu
363          165              170              175
365 agc gcc tgt ttg aat ctc acg gag cgt aaa cgg ttg gtg gcg cag cat     576
366 Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His
367          180              185              190
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VERIFICATION SUMMARY
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L:12 M:270 C: Current Application Number differs, Replaced Current Application No
L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date